

## SEQUENCE LISTING

5 <110> KUEHN, Ralf  
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 SCHWENK, Frieder  
 KUETER-LUKS, Birgit  
 FAUST, Nicole

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<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: primer C31-2-2

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<210> 12
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<213> Artificial Sequence

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<220>  
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25

35

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 tgtggaagt ccccaggctc cccagcaggc agaagtatgc aaagcatgca tctcaattag 180  
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<220>

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<222> (1)..(1839)

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	Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala	
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5	aca cag cgt agc gcc aac gaa gac aag gcg gcc gac ctt cag cgc gaa	144
	Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu	
	35 40 45	
0	gtc gag cgc gac ggg ggc cgg ttc agg ttc gtc ggg cat ttc agc gaa	192
	Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu	
	50 55 60	
0	gcg ccg ggc acg tcg gcg ttc ggg acg gcg gag cgc ccg gag ttc gaa	240
	Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu	
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5	cgc atc ctg aac gaa tgc cgc gcc ggg cgg ctc aac atg atc att gtc	288
	Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val	
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	Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro	
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45	att gtc tcg gaa ttg ctc gcc ctg ggc gtg acg att gtt tcc act cag	384
	Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln	
	115 120 125	
50	gaa ggc gtc ttc cgg cag gga aac gtc atg gac ctg att cac ctg att	432
	Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile	
	130 135 140	
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	Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys	
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60	att ctc gac acg aag aac ctt cag cgc gaa ttg ggc ggg tac gtc ggc	528
	Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly	
	165 170 175	
65	ggg aag gcg cct tac ggc ttc gag ctt gtt tcg gag acg aag gag atc	576
	Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile	
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65	acg cgc aac ggc cga atg gtc aat gtc gtc atc aac aag ctt gcg cac	624
	Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His	
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65	tcg acc act ccc ctt acc gga ccc ttc gag ttc gag ccc gac gta atc	672
	Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile	

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15	aag cgc atg gac gct gac gcc gtg ccg acc ccg ggc gag acg att ggg Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly 260 265 270	816		
20	aag aag acc gct tca agc gcc tgg gac ccg gca acc gtt atg cga atc Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile 275 280 285	864		
25	ctt ccg gac ccg cgt att gcg ggc ttc gcc gct gag gtg atc tac aag Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys 290 295 300	912		
30	aag aag ccg gac ggc acg ccg acc acg aag att gag ggt tac cgc att Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile 305 310 315 320	960		
35	cag cgc gac ccg atc acg ctc ccg ccg gtc gag ctt gat tgc gga ccg Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro 325 330 335	1008		
40	atc atc gag ccc gct gag tgg tat gag ctt cag gcg tgg ttg gac ggc Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly 340 345 350	1056		
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50	atg gac aag ctg tac tgc gag tgt ggc gcc gtc atg act tcg aag cgc Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg 370 375 380	1152		
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60	gtc gac ccg tcc gca cct ggg cag cac gaa ggc acg tgc aac gtc agc Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser 405 410 415	1248		
65	atg gcg gca ctc gac aag ttc gtt gcg gaa cgc atc ttc aac aag atc Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile 420 425 430	1296		
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85	gag ctg tac gaa gac cgc gcg gca ggc gcg tac gac gga ccc gtt ggc	1488		



Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly  
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5 agg aag cac ttc cgg aag caa cag gca gcg ctg acg ctc cgg cag caa 1536  
 Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln  
 500 505 510

10 ggg gcg gaa gag cgg ctt gcc gaa ctt gaa gcc gcc gaa gcc ccg aag 1584  
 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys  
 515 520 525

15 ctt ccc ctt gac caa tgg ttc ccc gaa gac gcc gac gct gac ccg acc 1632  
 Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr  
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ggc cct aag tcg tgg tgg ggg cgc gcg tca gta gac gac aag cgc gtg 1680  
 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val  
 545 550 555 560

20 ttc gtc ggg ctc ttc gta gac aag atc gtt gtc acg aag tcg act acg 1728  
 Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr  
 565 570 575

25 ggc agg ggg cag gga acg ccc atc gag aag cgc gct tcg atc acg tgg 1776  
 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp  
 580 585 590

30 ggc aag ccg ccg acc gac gac gac gaa gac gac gcc cag gac ggc acg 1824  
 Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr  
 595 600 605

35 gaa gac gta gcg gcg tag 1842  
 Glu Asp Val Ala Ala  
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 <213> Bacteriophage phi-C31

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50 Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu  
 35 40 45

Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu  
 50 55 60

55 Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu  
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60 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val  
 85 90 95

Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro  
 100 105 110

65 Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln  
 115 120 125

Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile

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	Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly 165 170 175		
10	Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile 180 185 190		
	Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His 195 200 205		
15	Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile 210 215 220		
0	Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys 225 230 235 240		
	Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys 245 250 255		
5	Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly 260 265 270		
	Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile 275 280 285		
10	Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys 290 295 300		
	Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile 305 310 315 320		
15	Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro 325 330 335		
40	Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly 340 345 350		
	Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala 355 360 365		
45	Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg 370 375 380		
	Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val 385 390 395 400		
50	Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser 405 410 415		
55	Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile 420 425 430		
	Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala 435 440 445		
60	Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu 450 455 460		
	Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu 465 470 475 480		
65	Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly 485 490 495		

Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln  
500 505 510

5 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys  
515 520 525

Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr  
530 535 540

10 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val  
545 550 555 560

Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr  
565 570 575

15 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp  
580 585 590

20 Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr  
595 600 605

Glu Asp Val Ala Ala  
610

25

<210> 22  
<211> 1863  
30 <212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: DNA sequence  
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<220>  
<221> CDS  
<222> (1)..(1860)

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45 gac cgt cag tcg cgc gag cgc gag aat tcg agc gca gca agc cca gcg 96  
Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala  
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50 aca cag cgt agc gcc aac gaa gac aag gcg gcc gac ctt cag cgc gaa 144  
Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu  
35 40 45

55 gtc gag cgc gac ggg ggc cgg ttc agg ttc gtc ggg cat ttc agc gaa 192  
Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu  
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60 gcg ccg ggc acg tcg gcg ttc ggg acg gcg gag cgc ccg gag ttc gaa 240  
Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu  
65 70 75 80

65 cgc atc ctg aac gaa tgc cgc gcc ggg cgg ctc aac atg atc att gtc 288  
Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val  
85 90 95

tat gac gtg tcg cgc ttc tcg cgc ctg aag gtc atg gac gcg att ccg 336  
Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro

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10	gaa ggc gtc ttc cgg cag gga aac gtc atg gac ctg att cac ctg att Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile 130 135 140	432		
15	atg cgg ctc gac gcg tgc cac aaa gaa tct tgc ctg aag tgc gcg aag Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys 145 150 155 160	480		
20	att ctc gac acg aag aac ctt cag cgc gaa ttg ggc ggg tac gtc ggc Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly 165 170 175	528		
25	ggg aag gcg cct tac ggc ttc gag ctt gtt tgc gag acg aag gag atc Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile 180 185 190	576		
30	acg cgc aac ggc cga atg gtc aat gtc gtc atc aac aag ctt gcg cac Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His 195 200 205	624		
35	tgc acc act ccc ctt acc gga ccc ttc gag ttc gag ccc gac gta atc Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile 210 215 220	672		
40	cgg tgg tgg tgg cgt gag atc aag acg cac aaa cac ctt ccc ttc aag Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys 225 230 235 240	720		
45	cgc ggc agt caa gcc gcc att cac ccg ggc agc atc acg ggc ctt tgt Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys 245 250 255	768		
50	aag cgc atg gac gct gac gcc gtg ccg acc ccg ggc gag acg att ggc Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly 260 265 270	816		
55	aag aag acc gct tca agc gcc tgg gac ccg gca acc gtt atg cga atc Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile 275 280 285	864		
60	ctt cgg gac ccg cgt att gcg ggc ttc gcc gct gag gtg atc tac aag Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys 290 295 300	912		
65	aag aag ccg gac ggc acg ccg acc acg aag att gag ggt tac cgc att Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile 305 310 315 320	960		
70	cag cgc gac ccg atc acg ctc cgg ccg gtc gag ctt gat tgc gga ccg Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro 325 330 335	1008		
75	atc atc gag ccc gct gag tgg tat gag ctt cag gcg tgg ttg gac ggc Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly 340 345 350	1056		
80	agg ggg cgc ggc aag ggg ctt tcc ccg ggg caa gcc att ctg tcc gcc Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala 355 360 365	1104		
85	atg gac aag ctg tac tgc gag tgt ggc gcc gtc atg act tgc aag cgc	1152		

65.  $\langle 210 \rangle$  23  
 $\langle 211 \rangle$  620  
 $\langle 212 \rangle$  PRT

<213> Artificial Sequence  
 <223> Description of Artificial Sequence: DNA sequence  
 coding for fusion protein C31-Int (CNLS)

5 <400> 23  
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10 Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala  
 20 25 30

Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu  
 35 40 45

15 Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu  
 50 55 60

Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu  
 65 70 75 80

20 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val  
 85 90 95

25 Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro  
 100 105 110

Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln  
 115 120 125

30 Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile  
 130 135 140

Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys  
 145 150 155 160

35 Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly  
 165 170 175

40 Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile  
 180 185 190

Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His  
 195 200 205

45 Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile  
 210 215 220

Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys  
 225 230 235 240

50 Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys  
 245 250 255

Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly  
 260 265 270

Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile  
 275 280 285

60 Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys  
 290 295 300

Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile  
 305 310 315 320

65 Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro  
 325 330 335

Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly  
 340 345 350  
 5 Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala  
 355 360 365  
 Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg  
 370 375 380  
 10 Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val  
 385 390 395 400  
 15 Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser  
 405 410 415  
 Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile  
 420 425 430  
 20 Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala  
 435 440 445  
 Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu  
 450 455 460  
 25 Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu  
 465 470 475 480  
 30 Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly  
 485 490 495  
 Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln  
 500 505 510  
 35 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys  
 515 520 525  
 Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr  
 530 535 540  
 40 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val  
 545 550 555 560  
 45 Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr  
 565 570 575  
 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp  
 580 585 590  
 50 Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr  
 595 600 605  
 Glu Asp Val Ala Ala Pro Lys Lys Lys Arg Lys Val  
 610 615 620  
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60 <210> 24  
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 <212> PRT  
 <213> Artificial Sequence

65 <220>  
 <223> Description of Artificial Sequence: NLS

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1

5

10

15

Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys  
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5

Lys Lys Lys Lys Arg Arg Arg Lys Thr Lys Arg  
           35                  40

10

<210> 25  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

15

<220>  
 <223> Description of Artificial Sequence: NLS

<400> 25  
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       1                  5                  10

0

<210> 26  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

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<220>  
 <223> Description of Artificial Sequence: NLS

30

<400> 26  
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35

<210> 27  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

40

<220>  
 <223> Description of Artificial Sequence: NLS

45

<400> 27  
 Met Thr Gly Ser Lys His Arg Lys His Pro Gly Ser Gly Ala  
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50

<210> 28  
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 <212> PRT  
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<220>  
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<400> 28  
 Gly Lys Lys Arg Ser Lys Ala  
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<210> 29  
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 <212> PRT  
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<220>



<400> 29

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<210> 30

&lt;211&gt; 11

&lt;212&gt; PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NLS

<400> 30

Ala Pro Lys Arg Lys Ser Gly Val Ser Lys Cys  
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<210> 31

<211> 12

&lt;212&gt; PRT

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence: NLS

<400> 31

Glu Glu Asp Gly Pro Gln Lys Lys Lys Arg Arg Leu  
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<210> 32

<211> 8

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: NLS

<400> 32

Ala Pro Thr Lys Arg Lys Gly Ser  
1 5

<210> 33

<211> 7

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence: NLS

<400> 33

Pro Asn Lys Lys Lys Arg Lys  
1 5

<210> 34

<211> 5

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence: NLS

<400> 34  
Lys Arg Pro Arg Pro  
1 5

5

<210> 35  
<211> 11  
<212> PRT  
<213> Artificial Sequence

10

<220>  
<223> Description of Artificial Sequence: NLS

<400> 35  
15 Cys Gly Gly Leu Ser Ser Lys Arg Pro Arg Pro  
1 5 10

0

<210> 36  
<211> 19  
<212> PRT  
<213> Artificial Sequence

5

<220>  
<223> Description of Artificial Sequence: NLS

<400> 36  
Pro Pro Lys Lys Arg Met Arg Arg Arg Ile Glu Pro Lys Lys Lys Lys  
1 5 10 15

0

Lys Arg Pro

5

<210> 37  
<211> 11  
<212> PRT  
<213> Artificial Sequence

40

<220>  
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<400> 37  
45 Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys  
1 5 10

50

<210> 38  
<211> 9  
<212> PRT  
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<220>  
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<400> 38  
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1 5

60

<210> 39  
<211> 9  
<212> PRT  
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<400> 39  
Ser Val Thr Lys Lys Arg Lys Leu Glu  
1 5  
5

<210> 40  
<211> 11  
<212> PRT  
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<220>  
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10 <210> 41  
<211> 9  
<212> PRT  
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5 <220>  
<223> Description of Artificial Sequence: NLS

10 <400> 41  
Pro Ala Ala Lys Arg Val Lys Leu Asp  
1 5

5 <210> 42  
<211> 11  
<212> PRT  
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40 <220>  
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45 <400> 42  
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50 <210> 43  
<211> 8  
<212> PRT  
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55 <220>  
<223> Description of Artificial Sequence: NLS

60 <400> 43  
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1 5

65 <210> 44  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NLS

<400> 44

Pro Leu Leu Lys Lys Ile Lys Gln  
1 5

5 <210> 45  
<211> 7  
<212> PRT  
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10 <220>  
<223> Description of Artificial Sequence: NLS

<400> 45  
Pro Gln Pro Lys Lys Lys Pro

15 1 5

<210> 46  
<211> 9  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: NLS

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Ser Lys Arg Val Ala Lys Arg Lys Leu  
1 5

10 <210> 47  
<211> 9  
<212> PRT  
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15 <220>  
<223> Description of Artificial Sequence: NLS

<400> 47  
Ala Ser Lys Ser Arg Lys Arg Lys Leu  
1 5

45 <210> 48  
<211> 16  
<212> PRT  
<213> Artificial Sequence

50 <220>  
<223> Description of Artificial Sequence: NLS

<400> 48  
Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu Leu Ala Thr  
1 5 10 15

55 <210> 49  
<211> 8  
<212> PRT  
60 <213> Artificial Sequence

<220>  
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65 <400> 49  
Arg Lys Thr Lys Lys Lys Ile Lys  
1 5

5 <210> 50  
<211> 8  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: NLS  
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<400> 50  
Arg Lys Leu Lys Lys Leu Gly Asn  
1 5  
  
15 <210> 51  
<211> 8  
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20  
<220>  
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<400> 51  
25 Arg Lys Asp Arg Arg Gly Gly Arg  
1 5  
  
30 <210> 52  
<211> 18  
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35 <223> Description of Artificial Sequence: NLS  
  
<400> 52  
Asp Thr Arg Glu Lys Lys Lys Phe Leu Lys Arg Arg Leu Leu Arg Leu  
1 5 10 15  
40 Asp Glu  
  
45 <210> 53  
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55 Pro Lys Lys Lys Arg Lys Val  
1 5  
  
60 <210> 54  
<211> 1410  
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<220>  
<221> CDS  
65 <222> (1)..(1407)  
  
<400> 54

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	Met Asn Arg Gly Gly Pro Thr Val Arg Ala Asp Ile Tyr Val Arg Ile	
	1 5 10 15	
5	agc ctg gac cgc aca ggg gaa gag ctc ggg gtc gag cgc cag gag gag	96
	Ser Leu Asp Arg Thr Gly Glu Glu Leu Gly Val Glu Arg Gln Glu Glu	
	20 25 30	
10	tcg tgt cgc gag ctc tgc aag agc ctc ggc atg gag gtg ggg cag gtg	144
	Ser Cys Arg Glu Leu Cys Lys Ser Leu Gly Met Glu Val Gly Gln Val	
	35 40 45	
15	tgg gtc gac aac gac ctg agc gcc acc aag aag aac gtc gtc cgc cct	192
	Trp Val Asp Asn Asp Leu Ser Ala Thr Lys Lys Asn Val Val Arg Pro	
	50 55 60	
	gac ttc gag gcg atg atc gcg agc aac ccg cag gcg atc gtc tgc tgg	240
	Asp Phe Glu Ala Met Ile Ala Ser Asn Pro Gln Ala Ile Val Cys Trp	
	65 70 75 80	
	cac acc gac cgg ctc atc cgc gtc acg cgg gac ctg gag cgg gtg atc	288
	His Thr Asp Arg Leu Ile Arg Val Thr Arg Asp Leu Glu Arg Val Ile	
	85 90 95	
5	gac ctc gga gtc aac gtc cac gcc gtg atg gcc gga cac ctg gac ctg	336
	Asp Leu Gly Val Asn Val His Ala Val Met Ala Gly His Leu Asp Leu	
	100 105 110	
30	tcc acc ccg gcc ggc cga gcc gtc gcc cgc acg gtg acg gcc tgg gcc	384
	Ser Thr Pro Ala Gly Arg Ala Val Ala Arg Thr Val Thr Ala Trp Ala	
	115 120 125	
35	acg tac gag ggc gag cag aag gct gag cgc cag aag ctc gcc aac atc	432
	Thr Tyr Glu Gly Glu Gln Lys Ala Glu Arg Gln Lys Leu Ala Asn Ile	
	130 135 140	
40	cag aac gcc cgc gcc ggc aag ccg tac acc ccc ggc atc cgc ccc ttc	480
	Gln Asn Ala Arg Ala Gly Lys Pro Tyr Thr Pro Gly Ile Arg Pro Phe	
	145 150 155 160	
	ggg tac ggc gac gac cac atg acc atc gtg acg gcc gag gcg gac gcc	528
	Gly Tyr Gly Asp His Met Thr Ile Val Thr Ala Glu Ala Asp Ala	
	165 170 175	
45	atc cgc gac ggc gcg aag atg atc ctc gac ggc tgg tcc ctg tcg gcc	576
	Ile Arg Asp Gly Ala Lys Met Ile Leu Asp Gly Trp Ser Leu Ser Ala	
	180 185 190	
50	gtg gct cgc tac tgg gag gag ctc aag ctc cag tcg ccc cgg agt atg	624
	Val Ala Arg Tyr Trp Glu Glu Leu Lys Leu Gln Ser Pro Arg Ser Met	
	195 200 205	
55	gcc gca ggc ggc aag ggc tgg tct ctg cgg ggc gta aag aag gtg ctg	672
	Ala Ala Gly Gly Lys Gly Trp Ser Leu Arg Gly Val Lys Lys Val Leu	
	210 215 220	
60	acc tcc ccg cgc tac gtc ggg cgg tcc agc tac ctc ggg gag gtc gtg	720
	Thr Ser Pro Arg Tyr Val Gly Arg Ser Ser Tyr Leu Gly Glu Val Val	
	225 230 235 240	
	ggc gat gct cag tgg ccg ccc atc ctc gac ccg gac gtc tac tac ggg	768
	Gly Asp Ala Gln Trp Pro Pro Ile Leu Asp Pro Asp Val Tyr Tyr Gly	
	245 250 255	
65	gtc gtg gcc atc ctg aac aac ccc gac cgc ttc agc ggg ggc cct cgg	816
	Val Val Ala Ile Leu Asn Asn Pro Asp Arg Phe Ser Gly Gly Pro Arg	
	260 265 270	

acc ggc cgc acc ccc ggc acg ctg ctc gca ggc atc gcc ttg tgc ggt 864  
 Thr Gly Arg Thr Pro Gly Thr Leu Leu Ala Gly Ile Ala Leu Cys Gly  
 275 280 285

5 gag tgc ggc aag acg gtc agt gga cgc ggc tac cga ggt gtc ctg gtc 912  
 Glu Cys Gly Lys Thr Val Ser Gly Arg Gly Tyr Arg Gly Val Leu Val  
 290 295 300

10 tac gga tgt aag gac acg cac act cgg acg cct cgg agc atc gct gac 960  
 Tyr Gly Cys Lys Asp Thr His Thr Arg Thr Pro Arg Ser Ile Ala Asp  
 305 310 315 320

15 ggc cgc ggc agc agc tcg acc ctc gcc cgg ctc atg ttc ccc gac ttc 1008  
 Gly Arg Ala Ser Ser Ser Thr Leu Ala Arg Leu Met Phe Pro Asp Phe  
 325 330 335

ctg ccc ggc ctc ctg gcc tct ggg cag gcc gag gac ggc cag tcg gca 1056  
 Leu Pro Gly Leu Leu Ala Ser Gly Gln Ala Glu Asp Gly Gln Ser Ala  
 340 345 350

gca tcc aag cac tcg gag gcc cag acg ctg cgc gag cgc ctt gac ggg 1104  
 Ala Ser Lys His Ser Glu Ala Gln Thr Leu Arg Glu Arg Leu Asp Gly  
 355 360 365

5 ctg gct acg gcc tac gcg gag ggt gcg atc agc ctg tct cag atg acg 1152  
 Leu Ala Thr Ala Tyr Ala Glu Gly Ala Ile Ser Leu Ser Gln Met Thr  
 370 375 380

10 gcc ggc tcg gaa gca ctg cgg aag aag ctg gag gtg atc gaa gcc gac 1200  
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 385 390 395 400

35 ctc gtg ggc tcg gca ggc atc ccg ccc ttc gat cca gtg gcc gga gtg 1248  
 Leu Val Gly Ser Ala Gly Ile Pro Pro Phe Asp Pro Val Ala Gly Val  
 405 410 415

40 gct ggc ctg atc tcc ggc tgg ccc acc acg cct ctc ccg acg cgt cga 1296  
 Ala Gly Leu Ile Ser Gly Trp Pro Thr Thr Pro Leu Pro Thr Arg Arg  
 420 425 430

gca tgg gtg gac ttc tgc ctg gtg gtc acg ctg aac acc cag aag ggg 1344  
 Ala Trp Val Asp Phe Cys Leu Val Val Thr Leu Asn Thr Gln Lys Gly  
 435 440 445

45 cgc cat gcg tcg agc atg acc gtg gac gac cac gtc acc atc gag tgg 1392  
 Arg His Ala Ser Ser Met Thr Val Asp Asp His Val Thr Ile Glu Trp  
 450 455 460

50 cga gac gtg gcc gag tag 1410  
 Arg Asp Val Ala Glu  
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55 <210> 55  
 <211> 469  
 <212> PRT  
 <213> Bacteriophage R4

60 <400> 55  
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65 Ser Leu Asp Arg Thr Gly Glu Glu Leu Gly Val Glu Arg Gln Glu Glu  
 20 25 30  
 Ser Cys Arg Glu Leu Cys Lys Ser Leu Gly Met Glu Val Gly Gln Val

	35	40	45
	Trp Val Asp Asn Asp Leu Ser Ala Thr Lys Lys Asn Val Val Arg Pro		
5	50	55	60
	Asp Phe Glu Ala Met Ile Ala Ser Asn Pro Gln Ala Ile Val Cys Trp		
	65	70	75
10	His Thr Asp Arg Leu Ile Arg Val Thr Arg Asp Leu Glu Arg Val Ile		
	85	90	95
	Asp Leu Gly Val Asn Val His Ala Val Met Ala Gly His Leu Asp Leu		
	100	105	110
15	Ser Thr Pro Ala Gly Arg Ala Val Ala Arg Thr Val Thr Ala Trp Ala		
	115	120	125
	Thr Tyr Glu Gly Glu Gln Lys Ala Glu Arg Gln Lys Leu Ala Asn Ile		
	130	135	140
0	Gln Asn Ala Arg Ala Gly Lys Pro Tyr Thr Pro Gly Ile Arg Pro Phe		
	145	150	155
5	Gly Tyr Gly Asp Asp His Met Thr Ile Val Thr Ala Glu Ala Asp Ala		
	165	170	175
	Ile Arg Asp Gly Ala Lys Met Ile Leu Asp Gly Trp Ser Leu Ser Ala		
	180	185	190
30	Val Ala Arg Tyr Trp Glu Glu Leu Lys Leu Gln Ser Pro Arg Ser Met		
	195	200	205
	Ala Ala Gly Gly Lys Gly Trp Ser Leu Arg Gly Val Lys Lys Val Leu		
	210	215	220
35	Thr Ser Pro Arg Tyr Val Gly Arg Ser Ser Tyr Leu Gly Glu Val Val		
	225	230	235
	Gly Asp Ala Gln Trp Pro Pro Ile Leu Asp Pro Asp Val Tyr Tyr Gly		
	245	250	255
40	Val Val Ala Ile Leu Asn Asn Pro Asp Arg Phe Ser Gly Gly Pro Arg		
	260	265	270
45	Thr Gly Arg Thr Pro Gly Thr Leu Leu Ala Gly Ile Ala Leu Cys Gly		
	275	280	285
	Glu Cys Gly Lys Thr Val Ser Gly Arg Gly Tyr Arg Gly Val Leu Val		
	290	295	300
50	Tyr Gly Cys Lys Asp Thr His Thr Arg Thr Pro Arg Ser Ile Ala Asp		
	305	310	315
	Gly Arg Ala Ser Ser Ser Thr Leu Ala Arg Leu Met Phe Pro Asp Phe		
	325	330	335
55	Leu Pro Gly Leu Leu Ala Ser Gly Gln Ala Glu Asp Gly Gln Ser Ala		
	340	345	350
60	Ala Ser Lys His Ser Glu Ala Gln Thr Leu Arg Glu Arg Leu Asp Gly		
	355	360	365
	Leu Ala Thr Ala Tyr Ala Glu Gly Ala Ile Ser Leu Ser Gln Met Thr		
	370	375	380
65	Ala Gly Ser Glu Ala Leu Arg Lys Lys Leu Glu Val Ile Glu Ala Asp		
	385	390	395
			400



Leu Val Gly Ser Ala Gly Ile Pro Pro Phe Asp Pro Val Ala Gly Val  
 405 410 415  
 5 Ala Gly Leu Ile Ser Gly Trp Pro Thr Thr Pro Leu Pro Thr Arg Arg  
 420 425 430  
 Ala Trp Val Asp Phe Cys Leu Val Val Thr Leu Asn Thr Gln Lys Gly  
 435 440 445  
 10 Arg His Ala Ser Ser Met Thr Val Asp Asp His Val Thr Ile Glu Trp  
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 25 <221> CDS  
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 gga tcg agc atc gac agc caa atc gag gcc tgt ata aag aaa gca ggg 96  
 Gly Ser Ser Ile Asp Ser Gln Ile Glu Ala Cys Ile Lys Lys Ala Gly  
 35 20 25 30  
 act aaa gat gtg ctg aag tat gca gat gaa gga ttt tca gga gag ctt 144  
 Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly Phe Ser Gly Glu Leu  
 35 40 45  
 40 tta gaa cgt ccg gct ttg aat cgc ttg agg gag gat gca agc aag gga 192  
 Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu Asp Ala Ser Lys Gly  
 50 55 60  
 45 ctt ata agt caa gtc att tgt tac gat cct gac cgt ctt tct cgg aaa 240  
 Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp Arg Leu Ser Arg Lys  
 65 70 75 80  
 tta atg aat cag cta atc att gat gac gaa ttg cga aag cga aac ata 288  
 Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu Arg Lys Arg Asn Ile  
 85 90 95  
 cct ttg att ttt gta aat ggt gaa tac gcc aat tct cca gaa ggt caa 336  
 Pro Leu Ile Phe Val Asn Gly Glu Tyr Ala Asn Ser Pro Glu Gly Gln  
 55 100 105 110  
 ttg ttt ttc gca atg cgc ggg gca atc tca gaa ttt gaa aaa gcc aaa 384  
 Leu Phe Phe Ala Met Arg Gly Ala Ile Ser Glu Phe Glu Lys Ala Lys  
 115 120 125  
 60 atc aaa gaa cgg aca tca agc ggc cga ctt caa aaa atg aaa aaa ggc 432  
 Ile Lys Glu Arg Thr Ser Ser Gly Arg Leu Gln Lys Met Lys Lys Gly  
 130 135 140  
 65 atg atc att aaa gat tct aaa cta tat ggc tat aaa ttt gtt aaa gag 480  
 Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr Lys Phe Val Lys Glu  
 145 150 155 160

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	Ile	Phe	Asn	Tyr	Phe	Thr	Asp	His	Lys	Ser	Pro	Phe	Phe	Gly	Arg	Val	
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	Gly	Ala	Lys	Val	Trp	His	Arg	Gln	Val	Val	Arg	Gln	Ile	Leu	Met	Asn	
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	Ser	Tyr	Val	Ser	Lys	Gln	Ala	Gly	Asn	Lys	Ser	Ile	Ile	Lys	Ile	Arg	
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	Pro	Glu	Glu	Glu	Gln	Ile	Thr	Val	Thr	Ile	Pro	Ala	Ile	Val	Pro	Ala	
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	Glu	Gln	Trp	Asp	Tyr	Ala	Gln	Glu	Leu	Leu	Gly	Gln	Ser	Lys	Arg	Lys	
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	His	Leu	Ser	Ile	Ser	Pro	His	Asn	Tyr	Leu	Leu	Ser	Gly	Leu	Val	Arg	
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	Gly	Lys	Asp	Tyr	Tyr	Val	Tyr	Thr	Cys	Arg	Lys	Asn	Tyr	Ser	Gly	Ala	
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	Lys	Asp	Arg	Gly	Cys	Gly	Lys	Glu	Met	Ser	Glu	Asn	Lys	Leu	Asn	Arg	
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	His	Val	Trp	Gly	Glu	Ile	Phe	Lys	Phe	Ile	Thr	Asn	Pro	Gln	Lys	Tyr	
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	Val	Ser	Phe	Lys	Glu	Ala	Glu	Gln	Ser	Asn	His	Leu	Ser	Asp	Glu	Leu	
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	Glu	Leu	Ile	Glu	Lys	Glu	Ile	Glu	Lys	Thr	Lys	Lys	Gly	Arg	Lys	Arg	
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75	ctt	tta	acg	cta	atc	agc	cta	agc	gat	gac	gat	gat	tta	gac	ata	gat	1248
	Leu	Leu	Thr	Leu	Ile	Ser	Leu	Ser	Asp	Asp	Asp	Asp	Leu	Asp	Ile	Asp	
					405					410					415		
80	gaa	atc	aaa	gca	caa	att	att	gaa	ctg	caa	aaa	aag	caa	aat	cag	ctt	1296
	Glu	Ile	Lys	Ala	Gln	Ile	Ile	Glu	Leu	Gln	Lys	Lys	Gln	Asn	Gln	Leu	

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 35    Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly Phe Ser Gly Glu Leu  
                  35                      40                      45  
 40    Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu Asp Ala Ser Lys Gly  
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      Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr Lys Phe Val Lys Glu  
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                  195                      200                      205

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	Asp Lys Gly Ala Leu Arg Lys Gln Ile Glu Arg Leu Arg Asn Ala Gly	
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	Cys Ser Lys Val Tyr Trp Asp Ile Gln Ser Arg Thr Thr Glu Val Arg	
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	Glu Gly Leu Gln Gln Leu Ile Asn Asp Leu Lys Thr Ser Ser Thr Gly	
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	Ser Arg Leu Phe Tyr Ser Leu Leu Glu Val Leu Arg Ser Lys Gly Ile	
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	Glu Leu Thr Ile Asp Met Leu Leu Ala Ala Lys Phe Glu Val Arg	
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	Phe Glu Cys Gly Ser Val Ala Ala Thr Val Arg Lys Leu His Ser Asp	
	195 200 205	
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	Phe Gly Ile Glu Thr Lys Val Leu Asn Trp Asn Lys Leu Glu Lys Ser	
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	Ser Arg Ile Val Gly Asp Asp Asp Leu Asp Lys Ile Ala Phe Thr Pro	
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	Asn Lys Thr Asn His Pro Leu Arg Tyr Pro Trp Ser Gly Leu Arg Trp	
	245 250 255	

	tca atc cct ggt tta aaa gcg tta tta gtt aac cct gtt tac gcc ggg	816
	Ser Ile Pro Gly Leu Lys Ala Leu Leu Val Asn Pro Val Tyr Ala Gly	
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	Gly Leu Pro Phe Asp Thr Tyr Val Lys Ser Lys Gly Lys Arg Lys His	
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	Phe Asp Glu Trp Lys Val Lys Trp Gly Thr His Asp Asp Glu Ala Ile	
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	Ile Thr Cys Glu Glu His Glu Arg Ile Lys Gln Met Ile Arg Asp Asn	
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	Ser Asn Leu Leu Lys Cys Thr His Cys Gly Gly Ser Met Thr Arg His	
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	Ala Lys Arg Val Asp Lys Ser Gly Gln Ala Ile Tyr Tyr Tyr Gln Cys	
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	Lys Ile Leu Asp Ile Gln Val Met Asp Leu Leu Ala Gln Glu Ala Glu	
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	ccc cca gaa gta aaa acg ctg cgc gca tcc ctg aat agt ctg gaa aca	1296
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	Gln Ile Ala Ile Ala Leu Gly Ala Thr Asn Asn Ala Ser Lys Gln Ser	
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	Trp Gln Gly Leu Asn Ala Gln Asp Lys Arg Ala Ile Leu Asn Gly Cys	
	485 490 495	
	gta aaa aaa atc tcc gta gat ggt aac ttt gtt aca gct att gag tat	1536
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	Val Lys Asp Met Ser Arg Leu Gly Arg Asn Tyr Leu Gln Val Gly Phe	
	85 90 95	
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	Tyr Thr Glu Val Leu Phe Pro Gln Lys Asn Val Arg Phe Leu Ala Ile	
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	Leu Val Val Asp Pro Val Ala Ser Glu Val Val Lys Arg Ile Phe Thr	
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	Ile Ile Ser Gln Glu Leu Trp Asp Ser Val Gln Lys Arg Arg Ser Arg	
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	Glu Val Lys Glu Arg Tyr Val Gly Pro Leu Ala Asp Val Val Glu Ser	
	35 40 45	
50	Tyr Leu Lys Met Lys Leu Gly Val Val Gly Asp Thr Pro Leu Gln Ala	
	50 55 60	
55	Asp Pro Pro Gly Phe Glu Pro Gly Thr Ser Gly Ser Gly Gly Gly Lys	
	65 70 75 80	
	Glu Gly Thr Glu Arg Arg Lys Ile Ala Leu Val Ala Asn Leu Arg Gln	
	85 90 95	
60	Tyr Ala Thr Asp Gly Asn Ile Lys Ala Phe Tyr Asn Tyr Leu Met Asn	
	100 105 110	
	Glu Arg Gly Ile Ser Glu Lys Thr Ala Lys Asp Tyr Ile Asn Ala Ile	
	115 120 125	
65	Ser Lys Pro Tyr Lys Glu Thr Arg Asp Ala Gln Lys Ala Tyr Arg Leu	
	130 135 140	

Phe Ala Arg Phe Leu Ala Ser Arg Asn Ile Ile His Asp Glu Phe Ala  
145 150 155 160

5 Asp Lys Ile Leu Lys Ala Val Lys Val Lys Lys Ala Asn Ala Asp Ile  
165 170 175

Tyr Ile Pro Thr Leu Glu Glu Ile Lys Arg Thr Leu Gln Leu Ala Lys  
180 185 190

10 Asp Tyr Ser Glu Asn Val Tyr Phe Ile Tyr Arg Ile Ala Leu Glu Ser  
195 200 205

15 Gly Val Arg Leu Ser Glu Ile Leu Lys Val Leu Lys Glu Pro Glu Arg  
210 215 220

Asp Ile Cys Gly Asn Asp Val Cys Tyr Tyr Pro Leu Ser Trp Thr Arg  
225 230 235 240

20 Gly Tyr Lys Gly Val Phe Tyr Val Phe His Ile Thr Pro Leu Lys Arg  
245 250 255

Val Glu Val Thr Lys Trp Ala Ile Ala Asp Phe Glu Arg Arg His Lys  
260 265 270

25 Asp Ala Ile Ala Ile Lys Tyr Phe Arg Lys Phe Val Ala Ser Lys Met  
275 280 285

Ala Glu Leu Ser Val Pro Leu Asp Ile Ile Asp Phe Ile Gln Gly Arg  
290 295 300

Lys Pro Thr Arg Val Leu Thr Gln His Tyr Val Ser Leu Phe Gly Ile  
305 310 315 320

35 Ala Lys Glu Gln Tyr Lys Lys Tyr Ala Glu Trp Leu Lys Gly Val  
325 330 335

40 <210> 66  
<211> 1441  
<212> DNA  
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45 <220>  
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coding for fusion protein NLS-XisA

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<222> (1)..(1437)

<400> 66

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caa caa gcc ttt gca gac tta gag cca ctt tca tct acc gac ggc agt 96  
Gln Gln Ala Phe Ala Asp Leu Glu Pro Leu Ser Ser Thr Asp Gly Ser  
20 25 30

60 ttt ctc ggc tca agt ctg caa gca cag cag caa aga gaa cac atg aga 144  
Phe Leu Gly Ser Ser Leu Gln Ala Gln Gln Gln Arg Glu His Met Arg  
35 40 45

65 aca aaa gta cta caa gac cta gac aag gta aat ctg cgt ttg aag tct 192  
Thr Lys Val Leu Gln Asp Leu Asp Lys Val Asn Leu Arg Leu Lys Ser

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5	gca aag acg aaa gtc tca gtt cga gaa tct aac gga agt ctg caa tta Ala Lys Thr Lys Val Ser Val Arg Glu Ser Asn Gly Ser Leu Gln Leu 65 70 75 80	240				
10	cga gca acg tta cca att aaa cct gga gat aag gac acc aac ggt aca Arg Ala Thr Leu Pro Ile Lys Pro Gly Asp Lys Asp Thr Asn Gly Thr 85 90 95	288				
15	ggc aga aag caa tac aat ctc agc ttg aat atc cct gca aac ttg gat Gly Arg Lys Gln Tyr Asn Leu Ser Leu Asn Ile Pro Ala Asn Leu Asp 100 105 110	336				
20	gga ctg aag acg gct gag gaa gaa gct tat gaa tta ggt aaa tta atc Gly Leu Lys Thr Ala Glu Glu Glu Ala Tyr Glu Leu Gly Lys Leu Ile 115 120 125	384				
25	gct cgg aaa acc ttt gaa tgg aat gat aaa tat tta ggc aaa gaa gcc Ala Arg Lys Thr Phe Glu Trp Asn Asp Lys Tyr Leu Gly Lys Glu Ala 130 135 140	432				
30	act aaa aaa gat tca caa aca ata ggt gat tta cta gaa aaa ttt gca Thr Lys Lys Asp Ser Gln Thr Ile Gly Asp Leu Leu Glu Lys Phe Ala 145 150 155 160	480				
35	gaa gag tat ttt aaa acc cat aaa cgc acc act aaa agc gaa cat acc Glu Glu Tyr Phe Lys Thr His Lys Arg Thr Thr Lys Ser Glu His Thr 165 170 175	528				
40	ttt ttt tac tat ttt tcc cgc acc caa cga tat acc aat tcc aaa gat Phe Phe Tyr Tyr Phe Ser Arg Thr Gln Arg Tyr Thr Asn Ser Lys Asp 180 185 190	576				
45	tta gca acg gcg gaa aat ctc atc aat tca att gag caa atc gat aaa Leu Ala Thr Ala Glu Asn Leu Ile Asn Ser Ile Glu Gln Ile Asp Lys 195 200 205	624				
50	gaa tgg gcg aga tat aat gcc gcc aga gcc ata tca gct ttt tgc ata Glu Trp Ala Arg Tyr Asn Ala Ala Arg Ala Ile Ser Ala Phe Cys Ile 210 215 220	672				
55	aca ttc aat ata gaa att gat ttg tcc cag tat tcc aaa atg cct gat Thr Phe Asn Ile Glu Ile Asp Leu Ser Gln Tyr Ser Lys Met Pro Asp 225 230 235 240	720				
60	cgc aat tcg cgc aac atc ccc aca gat gca gaa ata cta tca gga att Arg Asn Ser Arg Asn Ile Pro Thr Asp Ala Glu Ile Leu Ser Gly Ile 245 250 255	768				
65	acc aaa ttt gaa gac tat cta gtt acc aga gga aat caa gtt aat gaa Thr Lys Phe Glu Asp Tyr Leu Val Thr Arg Gly Asn Gln Val Asn Glu 260 265 270	816				
70	gat gta aaa gat agc tgg caa ctt tgg cgc tgg aca tat gga atg tta Asp Val Lys Asp Ser Trp Gln Leu Trp Arg Trp Thr Tyr Gly Met Leu 275 280 285	864				
75	gca gtt ttt ggt tta cgc ccc agg gaa att ttt att aac cct aat att Ala Val Phe Gly Leu Arg Pro Arg Glu Ile Phe Ile Asn Pro Asn Ile 290 295 300	912				
80	gat tgg tgg tta agc aaa gag aat ata gac ctc aca tgg aaa gta gac Asp Trp Trp Leu Ser Lys Glu Asn Ile Asp Leu Thr Trp Lys Val Asp 305 310 315 320	960				
85	aaa gaa tgt aaa act ggt gaa aga caa gca tta ccc tta cat aaa gaa	1008				

Lys Glu Cys Lys Thr Gly Glu Arg Gln Ala Leu Pro Leu His Lys Glu  
 325 330 335

5 tgg att gat gag ttt gat tta aga aat ccg aaa tat tta gaa atg ctg 1056  
 Trp Ile Asp Glu Phe Asp Leu Arg Asn Pro Lys Tyr Leu Glu Met Leu  
 340 345 350

10 gca aca gca att agt aaa aaa gat aaa aca aat cat gct gaa ata aca 1104  
 Ala Thr Ala Ile Ser Lys Lys Asp Lys Thr Asn His Ala Glu Ile Thr  
 355 360 365

15 gcc tta act cag cgt att agt tgg tgg ttt cgg aaa gtc gaa tta gat 1152  
 Ala Leu Thr Gln Arg Ile Ser Trp Trp Phe Arg Lys Val Glu Leu Asp  
 370 375 380

ttt aaa ccc tat gat tta cgt cac gcc tgg gca atc aga gcg cat att 1200  
 Phe Lys Pro Tyr Asp Leu Arg His Ala Trp Ala Ile Arg Ala His Ile  
 385 390 395 400

0 tta ggc ata cca atc aaa gcg gcg gct gat aat ttg ggg cat agt atg 1248  
 Leu Gly Ile Pro Ile Lys Ala Ala Ala Asp Asn Leu Gly His Ser Met  
 405 410 415

5 cag gtt cat aca caa acc tat cag cgc tgg ttc tcg cta gat atg cgg 1296  
 Gln Val His Thr Gln Thr Tyr Gln Arg Trp Phe Ser Leu Asp Met Arg  
 420 425 430

30 aag tta gcg att aat cag gct ttg act aag agg aat gaa ttt gag gtg 1344  
 Lys Leu Ala Ile Asn Gln Ala Leu Thr Lys Arg Asn Glu Phe Glu Val  
 435 440 445

35 att agg gag gag aat gct aaa ttg cag ata gaa aat gaa agg ttg agg 1392  
 Ile Arg Glu Glu Asn Ala Lys Leu Gln Ile Glu Asn Glu Arg Leu Arg  
 450 455 460

atg gaa att gag aag tta aag atg gaa ata gct tat aag aat agt tgag 1441  
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 <212> PRT  
 <213> Artificial Sequence

45 <223> Description of Artificial Sequence: DNA sequence  
 coding for fusion protein NLS-XisA

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 55 Phe Leu Gly Ser Ser Leu Gln Ala Gln Gln Gln Arg Glu His Met Arg  
 35 40 45  
 Thr Lys Val Leu Gln Asp Leu Asp Lys Val Asn Leu Arg Leu Lys Ser  
 50 55 60  
 60 Ala Lys Thr Lys Val Ser Val Arg Glu Ser Asn Gly Ser Leu Gln Leu  
 65 70 75 80  
 65 Arg Ala Thr Leu Pro Ile Lys Pro Gly Asp Lys Asp Thr Asn Gly Thr  
 85 90 95  
 Gly Arg Lys Gln Tyr Asn Leu Ser Leu Asn Ile Pro Ala Asn Leu Asp

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10	Thr	Lys	Lys	Asp	Ser	Gln	Thr	Ile	Gly	Asp	Leu	Leu	Glu	Lys	Phe	Ala	
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	Leu	Ala	Thr	Ala	Glu	Asn	Leu	Ile	Asn	Ser	Ile	Glu	Gln	Ile	Asp	Lys	
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20	Glu	Trp	Ala	Arg	Tyr	Asn	Ala	Ala	Arg	Ala	Ile	Ser	Ala	Phe	Cys	Ile	
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30	Thr	Lys	Phe	Glu	Asp	Tyr	Leu	Val	Thr	Arg	Gly	Asn	Gln	Val	Asn	Glu	
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	Asp	Val	Lys	Asp	Ser	Trp	Gln	Leu	Trp	Arg	Trp	Thr	Tyr	Gly	Met	Leu	
			275					280					285				
35	Ala	Val	Phe	Gly	Leu	Arg	Pro	Arg	Glu	Ile	Phe	Ile	Asn	Pro	Asn	Ile	
	290						295					300					
	Asp	Trp	Trp	Leu	Ser	Lys	Glu	Asn	Ile	Asp	Leu	Thr	Trp	Lys	Val	Asp	
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	Lys	Glu	Cys	Lys	Thr	Gly	Glu	Arg	Gln	Ala	Leu	Pro	Leu	His	Lys	Glu	
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45	Trp	Ile	Asp	Glu	Phe	Asp	Leu	Arg	Asn	Pro	Lys	Tyr	Leu	Glu	Met	Leu	
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	Ala	Thr	Ala	Ile	Ser	Lys	Lys	Asp	Lys	Thr	Asn	His	Ala	Glu	Ile	Thr	
			355					360					365				
50	Ala	Leu	Thr	Gln	Arg	Ile	Ser	Trp	Trp	Phe	Arg	Lys	Val	Glu	Leu	Asp	
	370						375					380					
	Phe	Lys	Pro	Tyr	Asp	Leu	Arg	His	Ala	Trp	Ala	Ile	Arg	Ala	His	Ile	
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					405					410					415		
60	Gln	Val	His	Thr	Gln	Thr	Tyr	Gln	Arg	Trp	Phe	Ser	Leu	Asp	Met	Arg	
				420					425					430			
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			435					440					445				
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aag cta gag tat gaa aac ggt gag gta aaa gag cgt tac gtg ggt cct 144  
 Lys Leu Glu Tyr Glu Asn Gly Glu Val Lys Glu Arg Tyr Val Gly Pro  
 35 40 45

35

tta gct gac gtc gtt gaa tca tat cta aaa atg aaa tta ggg gtc gta 192  
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40

ggg gat act ccc cta caa gcg gat ccc ccc ggt ttc gag ccc ggg aca 240  
 Gly Asp Thr Pro Leu Gln Ala Asp Pro Pro Gly Phe Glu Pro Gly Thr  
 65 70 75 80

agc gga agc ggt ggt gga aaa gag gga act gaa cga cgt aaa ata gcg 288  
 Ser Gly Ser Gly Gly Gly Lys Glu Gly Thr Thr Glu Arg Arg Lys Ile Ala  
 85 90 95

45

ttg gtt gcc aat ttg cgc caa tac gcg acg gac ggc aac ata aag gcg 336  
 Leu Val Ala Asn Leu Arg Gln Tyr Ala Thr Asp Gly Asn Ile Lys Ala  
 100 105 110

50

ttc tac aac tat ctc atg aac gaa agg ggg ata agc gaa aaa act gca 384  
 Phe Tyr Asn Tyr Leu Met Asn Glu Arg Gly Ile Ser Glu Lys Thr Ala  
 115 120 125

55

aag gac tac atc aat gct ata tca aag ccg tat aaa gag acg aga gac 432  
 Lys Asp Tyr Ile Asn Ala Ile Ser Lys Pro Tyr Lys Glu Thr Arg Asp  
 130 135 140

60

gca cag aag gct tac cga ctc ttt gca cgt ttc tta gcg tca cgc aat 480  
 Ala Gln Lys Ala Tyr Arg Leu Phe Ala Arg Phe Leu Ala Ser Arg Asn  
 145 150 155 160

atc ata cat gat gaa ttt gcg gat aaa ata ttg aaa gcg gta aag gtg 528  
 Ile Ile His Asp Glu Phe Ala Asp Lys Ile Leu Lys Ala Val Lys Val  
 165 170 175

65

aag aag gcg aac gct gat atc tac att cca acg ttg gaa gag ata aaa 576  
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 180 185 190

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	Arg	Thr	Leu	Gln	Leu	Ala	Lys	Asp	Tyr	Ser	Glu	Asn	Val	Tyr	Phe	Ile	
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10	gtg	ctg	aag	gaa	ccc	gaa	agg	gac	att	tgc	ggt	aac	gac	gtc	tgt	tat	720
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15	tat	ccg	ctt	agt	tgg	act	agg	gga	tat	aag	ggc	gtc	ttc	tat	gta	ttc	768
	Tyr	Pro	Leu	Ser	Trp	Thr	Arg	Gly	Tyr	Lys	Gly	Val	Phe	Tyr	Val	Phe	
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	Asp	Phe	Glu	Arg	Arg	His	Lys	Asp	Ala	Ile	Ala	Ile	Lys	Tyr	Phe	Arg	
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	Tyr	Val	Ser	Leu	Phe	Gly	Ile	Ala	Lys	Glu	Gln	Tyr	Lys	Lys	Tyr	Ala	
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1100144053 11112011

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 Lys Lys Ala Asn Ala Asp Ile Tyr Ile Pro Thr Leu Glu Glu Ile Lys  
 180 185 190  
 Arg Thr Leu Gln Leu Ala Lys Asp Tyr Ser Glu Asn Val Tyr Phe Ile  
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 210 215 220  
 Val Leu Lys Glu Pro Glu Arg Asp Ile Cys Gly Asn Asp Val Cys Tyr  
 225 230 235 240  
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 245 250 255  
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 260 265 270  
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&lt;211&gt; 3927

65. &lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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10 <213> Artificial Sequence

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50 &lt;211&gt; 4886

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&lt;220&gt;

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10 <211> 4905

<212> DNA

<213> Artificial Sequence

<220>

15 <223> Description of Artificial Sequence: vector  
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&lt;213&gt; Artificial Sequence

&lt;220&gt;

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51

65 &lt;210&gt; 85

&lt;211&gt; 76

&lt;212&gt; DNA

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<211> 82

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<210> 94

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65. &lt;211&gt; 20

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Ile Gly Lys Asp Ile Pro Trp Ser Tyr Arg Thr Leu Arg Gln Thr Leu  
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